

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

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This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-pm2-BN0080-270  
400-003-al2t3=2000-04-27&td=1)

Seq primer: puc 18 forward

High quality sequence start: 30

High quality sequence stop: 344.

FEATURES

source

1..344  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="BN0080"

/note="Organ: breast\_normal; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716) - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 75 a 92 c 76 g 101 t

ORIGIN

Alignment Scores:

Pred. No.: 0.003 Length: 344  
Score: 85.00 Matches: 16  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-10-000-039A-4 (1-16) x BE001610 (1-344)

QY 1 GluAlaPheLeuGlyPheSerTyrAlaProProThrAspSerPheLeu 16

Db 227 GAGGCTTCTAGCTTTCTCTATGCGCTCCACGACTCTTCTC 274

RESULT 2

AA377138

LOCUS

AA377138 346 bp mRNA linear EST 21-APR-1997

DEFINITION

Similar to serine/threonine kinase, mRNA sequence.

ACCESSION

AA377138

VERSION

AA377138.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 346)

AUTHORS

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fullmer, R.A., Bult

, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,

Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald

L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.I., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Pelligrino, S.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, X., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

96026280

7566098

Other\_ESTs: THC173211

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Bioinformatics

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Email: arkerlavet@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (http://www.tigr.org/tadb/hgi/hgi.html)

Seq primer: M13 Reverse

Location/Qualifiers

1..346

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="ATCC (inhost):181556"

/db\_xref="taxon:9606"

/dev\_stage="adult"

/clone\_lib="Small intestine I"

/note="Organ: small intestine; Vector: pBluescript SK-;

Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 80 a 93 c 74 g 97 t

ORIGIN

Alignment Scores:

Pred. No.: 0.00301 Length: 346  
Score: 85.00 Matches: 16  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-000-039A-4 (1-16) x AA377138 (1-346)

QY 1 GluAlaPheLeuGlyPheSerTyrAlaProProThrAspSerPheLeu 16

Db 157 GAGGCTTCTAGCTTTCTCTATGCGCTCCACGACTCTTCTC 204

RESULT 3

BI032559

LOCUS

BI032559

DEFINITION

CM3-NN0246-120101-535-b07 NN0246 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BI032559

VERSION

BI032559.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 376)

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., White

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Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 376)

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